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RAW SEQUENCE LISTING

DATE: 09/12/2002

PATENT APPLICATION: US/10/029,359A

TIME: 12:28:12

Input Set : A:\10806-156.ST25.txt

Output Set: N:\CRF4\09122002\J029359A.raw

3 <110> APPLICANT: Attersand, Anneli
 5 <120> TITLE OF INVENTION: Protein Cluster II
 7 <130> FILE REFERENCE: 10806-156
 9 <140> CURRENT APPLICATION NUMBER: 10/029,359A
 C--> 10 <141> CURRENT FILING DATE: 2002-08-30
 12 <160> NUMBER OF SEQ ID NOS: 6
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 299
 18 <212> TYPE: DNA
 19 <213> ORGANISM: HUMAN
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (21)..(299)
 24 <223> OTHER INFORMATION:
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 32 aaa tcc tgg ctg aat ttt tta acc ttc ctc tat gga tcg gca ata ggg 101
 33 Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly
 34 15 20 25
 36 ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt 149
 37 Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly
 38 30 35 40
 40 gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca 197
 41 Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser
 42 45 50 55
 44 gat gat aat gga cag aat cat cta gga gga caa atg aac ttc aat gca 245
 45 Asp Asp Asn Gly Gln Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala
 46 60 65 70 75
 48 gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc 293
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 50 80 85 90
 52 tat tag 299
 53 Tyr
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 58 <211> LENGTH: 92
 59 <212> TYPE: PRT
 60 <213> ORGANISM: HUMAN
 62 <400> SEQUENCE: 2
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 65 1 5 10 15

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68 Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly Phe Ile Leu Phe Ser
69          20          25          30
72 Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
73          35          40          45
76 Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
77          50          55          60
80 Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
81 65          70          75          80
84 Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu Tyr
85          85          90
88 <210> SEQ ID NO: 3
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91 <213> ORGANISM: HUMAN
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95 <222> LOCATION: (55)..(489)
96 <223> OTHER INFORMATION:
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101                                     Asn
102                                     1
104 aca ggt gtc act gac aaa ctc tat caa aag atg aaa att ctt tgc tgg          105
105 Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys Trp
106          5          10          15
108 att atg aca gga cct caa aat cta gaa aaa aag atc aga cgc atc aga          153
109 Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile Arg
110          20          25          30
112 gat aca tgg gcc cag ggt tgc aat aaa gcg ttg ttt atg agc tca aaa          201
113 Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser Lys
114          35          40          45
116 gaa aat aaa gac ttc tct act gtg gga tta cac acc aaa gaa gac aga          249
117 Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp Arg
118 50          55          60          65
120 aac caa ctg tcc tgg aaa ata gtt aaa gct ttt cta tat gct cat gac          297
121 Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His Asp
122          70          75          80
124 cat tat ctg gaa tac atg gat tgg ttc atg aaa gca gat gat gat ata          345
125 His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp Ile
126          85          90          95
128 tgt ata tat atc aca ttg gac aac ttg aaa tgg ctt ctc aca aac tat          393
129 Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn Tyr
130          100          105          110
132 aac cct gat gaa tcc act tac ttt ggg aaa aga ttt aag cac tgc aga          441
133 Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys Arg
134          115          120          125
136 aaa cag gac tac atg act gga gga gca gga tat gta ctg agc aaa gaa          489
137 Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu
138 130          135          140          145

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152 Trp Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile
153 20 25 30
156 Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser
157 35 40 45
160 Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp
161 50 55 60
164 Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His
165 65 70 75 80
168 Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp
169 85 90 95
172 Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn
173 100 105 110
176 Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
177 115 120 125
180 Arg Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys
181 130 135 140
184 Glu
185 145

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196 <223> OTHER INFORMATION:
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201 Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn Phe Asn Ala Asp
202 1 5 10 15
204 tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat 97
205 Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
206 20 25 30
208 cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta 145
209 Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
210 35 40 45
212 gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac 193
213 Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
214 50 55 60
216 aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg 241
217 Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
218 65 70 75 80

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220 gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att      289
221 Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
222      85      90      95
224 aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg      337
225 Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
226      100      105      110
228 ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg      385
229 Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
230      115      120      125
232 tgg ctt ctt tca aaa tac gac cct gaa gaa ccc att tac ttt ggg aga      433
233 Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
234      130      135      140
236 aga ttt aag cct tat gta aag cag ggc tac atg agt gga gga gca gga      481
237 Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
238 145      150      155      160
240 tat gta cta agc aaa gaa gcc ttg aaa aga ttt gtt gat gca ttt aaa      529
241 Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
242      165      170      175
244 aca gac aag tgt aca cat agt tcc tcc att gaa gac tta gca ctg ggg      577
245 Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
246      180      185      190
248 aga tgc atg gaa att atg aat gta gaa gca gga gat tcc aga gat acc      625
249 Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
250      195      200      205
252 att gga aaa gaa act ttt cat ccc ttt gtg cca gaa cac cat tta att      673
253 Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
254      210      215      220
256 aaa ggt tat cta cct aga acg ttt tgg tac tgg aat tac aac tat tat      721
257 Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
258 225      230      235      240
260 cct cct gta gag ggt cct ggt tgc tgc tct gat ctt gca gtt tct ttt      769
261 Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
262      245      250      255
264 cac tat gtt gat tct aca acc atg tat gag tta gaa tac ctc gtt tat      817
265 His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
266      260      265      270
268 cat ctt cgt cca tat ggt tat tta tac aga tat caa cct acc tta cct      865
269 His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
270      275      280      285
272 gaa cgt ata cta aag gaa att agt caa gca aac aaa aat gaa gat aca      913
273 Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
274      290      295      300
276 aaa gtg aag tta gga aat cct tgaaagaaaa tcatgaatga acaaaggtaa      964
277 Lys Val Lys Leu Gly Asn Pro
278 305      310
280 tatgtctagc actgcactga aaaaggactt ctgcatttct gacatagaac actggaatcc      1024
282 cagtgaggaa ttctaagtga acattcctta tagaaacctt tcacatgaat gactataaac      1084
284 tgaagcttta aatgagctgt gaagtgtgtt aaaatgtgtt ttgatacagt aatatataaa      1144
286 tatgtctata tatatgagga acttgtgttt tttaaagtgt ggccaggtag aggaactaga      1204

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292 aagaaaaattt tagaaagaaa tattgttgct cagtgttggt aatatagctc aagaattgag 1384
294 tttatatattg cagtatgcta taaatgatac cccctacca caccacaca cacagttttt 1444
296 gtctaatagaa aatgttgctg tgattattta taattggtag tatttcttcc agaagaagct 1504
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303 <212> TYPE: PRT
304 <213> ORGANISM: HUMAN
306 <400> SEQUENCE: 6
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312 Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
313 20 25 30
316 Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
317 35 40 45
320 Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
321 50 55 60
324 Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
325 65 70 75 80
328 Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
329 85 90 95
332 Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
333 100 105 110
336 Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
337 115 120 125
340 Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
341 130 135 140
344 Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
345 145 150 155 160
348 Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
349 165 170 175
352 Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
353 180 185 190
356 Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
357 195 200 205
360 Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
361 210 215 220
364 Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
365 225 230 235 240
368 Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
369 245 250 255
372 His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
373 260 265 270
376 His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
377 275 280 285
380 Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
381 290 295 300

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VERIFICATION SUMMARY

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